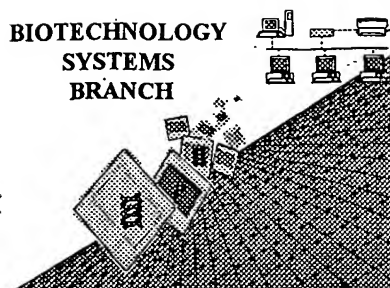0400

BEST AVAILABLE COPY

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/015,989_

Source: _OIPE_

Date Processed by STIC: _1/3/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE: SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _10/015,989_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1 ____ Wrapped Nucleics
      Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
      Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
      "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
      (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
      (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
      (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
      Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
      "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

          Input Set : A:\ES.txt
          Output Set: N:\CRF3\01032002\J015989.raw

```
    7 <110> APPLICANT: DARROW, ANDREW
   10         QI, JENSON
   13         ANDRADE-GORDON, PATRICIA
   19 <120> TITLE OF INVENTION: ZYMOGEN ACTIVATION SYSTEM
   25 <130> FILE REFERENCE: ORT-1552
   31 <140> CURRENT APPLICATION NUMBER: US/10/015,989
   34 <141> CURRENT FILING DATE: 2001-12-10
   40 <160> NUMBER OF SEQ ID NOS: 60
   46 <170> SOFTWARE: PATENTIN VER. 2.0
```

see item 4 on Error Summary Sheet

Does Not Comply *pp 1-12*
Corrected Diskette Needed

ERRORED SEQUENCES

FYI! nucleotides must be in lower-case letters, when Sequence Listing is in new Sequence Rules format

```
   52 <210> SEQ ID NO: 1
   55 <211> LENGTH: 361
   58 <212> TYPE: DNA
   61 <213> ORGANISM: ARTIFICIAL SEQUENCE
   67 <220> FEATURE:
   70 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
   73         VECTORS.
   79 <400> SEQUENCE: 1
E--> 82 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
   83 cctgctgctg 60
E--> 86 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
   87 cgacgacgac 120
E--> 90 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
   91 tgggggctat 180
E--> 94 gctctagata gcggccgctt cccctttagtg agggttaatg cttcgagcag
   95 acatgataag 240
E--> 98 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat
   99 gctttatttg 300
E--> 102 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata
   103 aacaagttga 360
   106 c                                                        361
   112 <210> SEQ ID NO: 2
   115 <211> LENGTH: 301
   118 <212> TYPE: DNA
   121 <213> ORGANISM: ARTIFICIAL SEQUENCE
   127 <220> FEATURE:
   130 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
   133         VECTORS.
   139 <400> SEQUENCE: 2
E--> 142 gaattcacca tgaatccact cctgatcctt acctttgtgg cggccgctct
   143 tgctgccccc 60
E--> 146 tttgatgatg atgacaagat cgttgggggc tattgtctag atacccctac
   147 gatgtgcccg 120
E--> 150 attacgccta gcggccgctt cccctttagtg agggttaatg cttcgagcag
```

→ 60 ← format (see error item 1 on Error Summary Sheet)

→ 120 ←

same format error

```
       151 acatgataag 180
E--> 154 atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaat
       155 gctttatttg 240
E--> 158 tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata
       159 aacaagttga 300
       162 c                                               301
       168 <210> SEQ ID NO: 3
       171 <211> LENGTH: 484
       174 <212> TYPE: DNA
       177 <213> ORGANISM: ARTIFICIAL SEQUENCE
       183 <220> FEATURE:
       186 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
       189       VECTORS.
       195 <400> SEQUENCE: 3
E--> 198 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
       199 cctgctgctg 60
E--> 202 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
       203 cgacgacgac 120
E--> 206 gtggacgcgg ccgctcttgc tgcccccttt atcgaggggc gcattgtgga
       207 gggctcggat 180
E--> 210 ctagataccc ctacgatgtg cccgattacg ccgctagata cccctacgat
       211 gtgcccgatt 240
E--> 214 acgccgctag ataccactac gatgtgcccg attacgccgc tagataccccc
       215 tacgatgtgc 300
E--> 218 ccgattacgc ctagcggccg cttccctta gtgagggtta atgcttcgag
       219 cagacatgat 360
E--> 222 aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa
       223 aatgctttat 420
E--> 226 ttgtgaaatt tgtgatgcta ttgctttatt tgtaaccatt ataagctgca
       227 ataaacaagt 480
       230 tgac                                            484
       236 <210> SEQ ID NO: 4
       239 <211> LENGTH: 382
       242 <212> TYPE: DNA
       245 <213> ORGANISM: ARTIFICIAL SEQUENCE
       251 <220> FEATURE:
       254 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
       257       VECTORS.
       263 <400> SEQUENCE: 4
E--> 266 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
       267 cctgctgctg 60
E--> 270 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
       271 cgacgacgac 120
E--> 274 gtggacgcgg ccgctcttgc tgccccctt gatgatgatg acaagatcgt
       275 tggggctac 180
E--> 278 aactgtctag acatcaccat caccatcact agcggccgct tcccttagt
       279 gagggttaat 240
E--> 282 gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa
       283 ctagaatgca 300
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01032002\J015989.raw**

```
E--> 286 gtgaaaaaaa tgctttattt gtgaaatttg tgatgctatt gctttatttg      same
     287 taaccattat 360
     290 aagctgcaat aaacaagttg ac                                        382
     296 <210> SEQ ID NO: 5
     299 <211> LENGTH: 352
     302 <212> TYPE: DNA
     305 <213> ORGANISM: ARTIFICIAL SEQUENCE
     311 <220> FEATURE:
     314 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     317       VECTORS.
     323 <400> SEQUENCE: 5
E--> 326 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
     327 gggtaccacc 60
E--> 330 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
     331 tgctgccccc 120                                                same
E--> 334 tttgatgatg atgacaagat cgttgggggc tatgctctag acatcaccat
     335 caccatcact 180
E--> 338 agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa
     339 gatacattga 240
E--> 342 tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa tgctttattt
     343 gtgaaatttg 300
E--> 346 tgatgctatt gctttatttg taaccattat aagctgcaat aaacaagttg
     347 ac          352
     353 <210> SEQ ID NO: 6
     356 <211> LENGTH: 385
     359 <212> TYPE: DNA
     362 <213> ORGANISM: ARTIFICIAL SEQUENCE
     368 <220> FEATURE:
     371 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     374       VECTORS.
     380 <400> SEQUENCE: 6
E--> 383 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
     384 gggtaccacc 60
E--> 387 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
     388 tgctgccccc 120
E--> 391 tttgatgatg atgacaagat cgttgggggc tatgctctag atacccctac
     392 gatgtgcccg 180                                                same
E--> 395 attacgccgc tagacatcac catcaccatc actagcggcc gcttcccttt
     396 agtgagggtt 240
E--> 399 aatgcttcga gcagacatga taagatacat tgatgagttt ggacaaacca
     400 caactagaat 300
E--> 403 gcagtgaaaa aaatgcttta tttgtgaaat ttgtgatgct attgctttat
     404 ttgtaaccat 360
     407 tataagctgc aataaacaag ttgac                                     385
     413 <210> SEQ ID NO: 7
     416 <211> LENGTH: 1169
     419 <212> TYPE: DNA
     422 <213> ORGANISM: ARTIFICIAL SEQUENCE
     428 <220> FEATURE:
```

```
        431 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
        434       WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
        440 <400> SEQUENCE: 7
E--> 443 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
     444 cctgctgctg 60
E--> 447 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
     448 cgacgacgac 120
E--> 451 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
     452 tgggggctat 180
E--> 455 gctctagagg ccggtcagtg gccctggcag gtcagcatca cctatgaagg
     456 cgtccatgtg 240
E--> 459 tgtggtggct ctctcgtgtc tgagcagtgg gtgctgtcag ctgctcactg
     460 cttccccagc 300
E--> 463 gagcaccaca aggaagccta tgaggtcaag ctggggccc accagctaga
     464 ctcctactcc 360
E--> 467 gaggacgcca aggtcagcac cctgaaggac atcatccccc accccagcta
     468 cctccaggag 420
E--> 471 ggctcccagg gcgacattgc actcctccaa ctcagcagac ccatcacctt
     472 ctcccgctac 480
E--> 475 atccggccca tctgcctccc tgcagccaac gcctccttcc ccaacggcct
     476 ccactgcact 540
E--> 479 gtcactggct ggggtcatgt ggccccctca gtgagcctcc tgacgcccaa
     480 gccactgcag 600
E--> 483 caactcgagg tgcctctgat cagtcgtgag acgtgtaact gcctgtacaa
     484 catcgacgcc 660
E--> 487 aagcctgagg agccgcactt tgtccaagag gacatggtgt gtgctggcta
     488 tgtggagggg 720
E--> 491 ggcaaggacg cctgccaggg tgactctggg gcccactct cctgccctgt
     492 ggagggtctc 780
E--> 495 tggtacctga cgggcattgt gagctgggga gatgcctgtg gggcccgcaa
     496 caggcctggt 840
E--> 499 gtgtacactc tggcctccag ctatgcctcc tggatccaaa gcaaggtgac
     500 agaactccag 900
E--> 503 cctcgtgtgg tgccccaaac ccaggagtcc cagcccgaca gcaacctctg
     504 tggcagccac 960
E--> 507 ctggccttca gctctagaca tcaccatcac catcactagc ggccgcttcc
     508 ctttagtgag 1020
E--> 511 ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa
     512 accacaacta 1080
E--> 515 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct
     516 ttatttgtaa 1140
     519 ccattataag ctgcaataaa caagttgac                          1169
     525 <210> SEQ ID NO: 8
     528 <211> LENGTH: 1142
     531 <212> TYPE: DNA
     534 <213> ORGANISM: ARTIFICIAL SEQUENCE
     540 <220> FEATURE:
     543 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
     546       WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
```

same

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989 TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
      552 <400> SEQUENCE: 8
E--> 555 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
      556 gggtaccacc 60
E--> 559 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
      560 tgctgccccc 120
E--> 563 tttgatgatg atgacaagat cgttgggggc tatgctctag aggccggtca
      564 gtggccctgg 180
E--> 567 caggtcagca tcacctatga aggcgtccat gtgtgtggtg gctctctcgt
      568 gtctgagcag 240
E--> 571 tgggtgctgt cagctgctca ctgcttcccc agcgagcacc acaaggaagc
      572 ctatgaggtc 300
E--> 575 aagctggggg cccaccagct agactcctac tccgaggacg ccaaggtcag
      576 caccctgaag 360
E--> 579 gacatcatcc cccaccccag ctacctccag gagggctccc agggcgacat
      580 tgcactcctc 420
E--> 583 caactcagca gacccatcac cttctcccgc tacatccggc ccatctgcct
      584 ccctgcagcc 480
E--> 587 aacgcctcct tccccaacgg cctccactgc actgtcactg gctggggtca
      588 tgtggccccc 540
E--> 591 tcagtgagcc tcctgacgcc caagccactg cagcaactcg aggtgcctct
      592 gatcagtcgt 600
E--> 595 gagacgtgta actgcctgta caacatcgac gccaagcctg aggagccgca
      596 ctttgtccaa 660
E--> 599 gaggacatgg tgtgtgctgg ctatgtggag ggggcaagg acgcctgcca
      600 gggtgactct 720
E--> 603 gggggcccac tctcctgccc tgtggagggt ctctggtacc tgacgggcat
      604 tgtgagctgg 780
E--> 607 ggagatgcct gtggggcccg caacaggcct ggtgtgtaca ctctggcctc
      608 cagctatgcc 840
E--> 611 tcctggatcc aaagcaaggt gacagaactc cagcctcgtg tggtgcccca
      612 aacccaggag 900
E--> 615 tcccagcccg acagcaacct ctgtggcagc cacctggcct tcagctctag
      616 acatcaccat 960
E--> 619 caccatcact agcggccgct ccctttagt gagggttaat gcttcgagca
      620 gacatgataa 1020
E--> 623 gatacattga tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaa
      624 tgctttatttt 1080
E--> 627 gtgaaatttg tgatgctatt gctttatttg taaccattat aagctgcaat
      628 aaacaagttg 1140
      631 ac                                                    1142
      637 <210> SEQ ID NO: 9
      640 <211> LENGTH: 1049
      643 <212> TYPE: DNA
      646 <213> ORGANISM: ARTIFICIAL SEQUENCE
      652 <220> FEATURE:
      655 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      658          WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
      664 <400> SEQUENCE: 9
E--> 667 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
```

same

same

```
        668 cctgctgctg 60
E--> 671 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
        672 cgacgacgac 120
E--> 675 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
        676 tggggctac 180
E--> 679 aactgtctag aaccccattc gcagccttgg caggcggcct tgttccaggg
        680 ccagcaacta 240
E--> 683 ctctgtggcg gtgtccttgt aggtggcaac tgggtcctta cagctgccca
        684 ctgtaaaaaa 300
E--> 687 ccgaaataca cagtacgcct gggagaccac agcctacaga ataaagatgg
        688 cccagagcaa 360
E--> 691 gaaatacctg tggttcagtc catcccacac ccctgctaca acagcagcga
        692 tgtggaggac 420
E--> 695 cacaaccatg atctgatgct tcttcaactg cgtgaccagg catccctggg
        696 gtccaaagtg 480
E--> 699 aagcccatca gcctggcaga tcattgcacc cagcctggcc agaagtgcac
        700 cgtctcaggc 540
E--> 703 tggggcactg tcaccagtcc ccgagagaat tttcctgaca ctctcaactg
        704 tgcagaagta 600
E--> 707 aaaatctttc cccagaagaa gtgtgaggat gcttacccgg ggcagatcac
        708 agatggcatg 660
E--> 711 gtctgtgcag gcagcagcaa aggggctgac acgtgccagg gcgattctgg
        712 aggcccccctg 720
E--> 715 gtgtgtgatg gtgcactcca gggcatcaca tcctggggct cagacccctg
        716 tgggaggtcc 780
E--> 719 gacaaacctg gcgtctatac caacatctgc cgctacctgg actggatcaa
        720 gaagatcata 840
E--> 723 ggcagcaagg gctctagaca tcaccatcac catcactagc ggccgcttcc
        724 ctttagtgag 900
E--> 727 ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa
        728 accacaacta 960
E--> 731 gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct
        732 ttatttgtaa 1020
        735 ccattataag ctgcaataaa caagttgac                          1049
        741 <210> SEQ ID NO: 10
        744 <211> LENGTH: 1052
        747 <212> TYPE: DNA
        750 <213> ORGANISM: ARTIFICIAL SEQUENCE
        756 <220> FEATURE:
        759 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
        762        WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
        768 <400> SEQUENCE: 10
E--> 771 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct
        772 cctgctgctg 60
E--> 775 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga
        776 cgacgacgac 120
E--> 779 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt
        780 tggggctac 180
E--> 783 aactgtctag aaaagcactc ccagccctgg caggcagccc tgttcgagaa
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
       784 gacgcggcta 240
E--> 787 ctctgtgggg cgacgctcat cgcccccaga tggctcctga cagcagccca
       788 ctgcctcaag 300
E--> 791 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg
       792 ctgtgagcag 360
E--> 795 acccggacag ccactgagtc cttcccccac cccggcttca acaacagcct
       796 ccccaacaaa 420
E--> 799 gaccaccgca atgacatcat gctggtgaag atggcatcgc cagtctccat
       800 cacctgggct 480
E--> 803 gtgcgacccc tcaccctctc ctcacgctgt gtcactgctg gcaccagctg
       804 cctcatttcc 540
E--> 807 ggctggggca gcacgtccag cccccagtta cgcctgcctc acaccttgcg
       808 atgcgccaac 600
E--> 811 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat
       812 cacagacacc 660
E--> 815 atggtgtgtg ccagcgtgca ggaagggggc aaggactcct gccagggtga
       816 ctccgggggc 720
E--> 819 cctctggtct gtaaccagtc tcttcaaggc attatctcct ggggccagga
       820 tccgtgtgcg 780
E--> 823 atcacccgaa agcctggtgt ctacacgaaa gtctgcaaat atgtggactg
       824 gatccaggag 840
E--> 827 acgatgaaga acaattctag acatcaccat caccatcact agcggccgct
       828 tccctttagt 900
E--> 831 gagggttaat gcttcgagca gacatgataa gatacattga tgagtttgga
       832 caaaccacaa 960
E--> 835 ctagaatgca gtgaaaaaaa tgctttattt gtgaaatttg tgatgctatt
       836 gctttatttg 1020
       839 taaccattat aagctgcaat aaacaagttg ac                     1052
      1067 <210> SEQ ID NO: 12
      1070 <211> LENGTH: 319
      1073 <212> TYPE: PRT
      1076 <213> ORGANISM: ARTIFICIAL SEQUENCE
      1082 <220> FEATURE:
      1085 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
      1088       WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
      1094 <400> SEQUENCE: 12
      1097 MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR
      1100  1               5                  10                  15
      1106 PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA
      1109             20                  25                  30
      1115 LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA
      1118             35                  40                  45
      1124 LEU GLU ALA GLY GLN TRP PRO TRP GLN VAL SER ILE THR TYR GLU GLY
      1127       50                  55                  60
      1133 VAL HIS VAL CYS GLY GLY SER LEU VAL SER GLU GLN TRP VAL LEU SER
      1136   65                  70                  75                  80
      1142 ALA ALA HIS CYS PHE PRO SER GLU HIS HIS LYS GLU ALA TYR GLU VAL
      1145             85                  90                  95
      1151 LYS LEU GLY ALA HIS GLN LEU ASP SER TYR SER GLU ASP ALA LYS VAL
```

same

see P. 8, too

Per Sequence Rules (1.822) only the first letter of amino acid is in upper-case. e.g. Met Ala

```
1154                 100              105              110
1160 SER THR LEU LYS ASP ILE ILE PRO HIS PRO SER TYR LEU GLN GLU GLY
1163              115              120              125
1169 SER GLN GLY ASP ILE ALA LEU LEU GLN LEU SER ARG PRO ILE THR PHE
1172      130              135              140
1178 SER ARG TYR ILE ARG PRO ILE CYS LEU PRO ALA ALA ASN ALA SER PHE
1181 145              150              155              160
1187 PRO ASN GLY LEU HIS CYS THR VAL THR GLY TRP GLY HIS VAL ALA PRO
1190              165              170              175
1196 SER VAL SER LEU LEU THR PRO LYS PRO LEU GLN GLN LEU GLU VAL PRO
1199              180              185              190
1205 LEU ILE SER ARG GLU THR CYS ASN CYS LEU TYR ASN ILE ASP ALA LYS
1208              195              200              205
1214 PRO GLU GLU PRO HIS PHE VAL GLN GLU ASP MET VAL CYS ALA GLY TYR
1217      210              215              220
1223 VAL GLU GLY GLY LYS ASP ALA CYS GLN GLY ASP SER GLY GLY PRO LEU
1226 225              230              235              240
1232 SER CYS PRO VAL GLU GLY LEU TRP TYR LEU THR GLY ILE VAL SER TRP
1235              245              250              255
1241 GLY ASP ALA CYS GLY ALA ARG ASN ARG PRO GLY VAL TYR THR LEU
1242 ALA
1245              260              265              270
1251 SER SER TYR ALA SER TRP ILE GLN SER LYS VAL THR GLU LEU GLN PRO
1254              275              280              285
1260 ARG VAL VAL PRO GLN THR GLN GLU SER GLN PRO ASP SER ASN LEU CYS
1263      290              295              300
1269 GLY SER HIS LEU ALA PHE SER SER ARG HIS HIS HIS HIS HIS HIS
1272 305              310              315
2409 <210> SEQ ID NO: 35
2412 <211> LENGTH: 55
2415 <212> TYPE: DNA
2418 <213> ORGANISM: ARTIFICIAL SEQUENCE
2424 <220> FEATURE:
2427 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2430       OLIGONUCLEOTIDE
2436 <400> SEQUENCE: 35
2439 aattcaccac catggctttc ctctggctcc tctcctgctg ggccctcctg
2440 ggtac        55
2446 <210> SEQ ID NO: 36
2449 <211> LENGTH: 47
2452 <212> TYPE: DNA
2455 <213> ORGANISM: ARTIFICIAL SEQUENCE
2461 <220> FEATURE:
2464 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2467       OLIGONUCLEOTIDE
2473 <400> SEQUENCE: 36
2476 ccaggagggc ccagcaggag aggagccaga ggaaagccat ggtggtg
2477 47
2483 <210> SEQ ID NO: 37
```

E--> markers appear at lines 1242, 1245, 1254, 1263, 1272, 2439, and 2476.

Handwritten annotations: "convert last two letters of amino acids to lower-case letters"; "move up"; "move up — see item 1 on Error summary sheet"; "same error".

```
         2486 <211> LENGTH: 45
         2489 <212> TYPE: DNA
         2492 <213> ORGANISM: ARTIFICIAL SEQUENCE
         2498 <220> FEATURE:
         2501 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
         2504      OLIGONUCLEOTIDE
         2510 <400> SEQUENCE: 37
E--> 2513 caccttcggc tgcggggtcc ccgactacaa ggacgacgac gacgc        same
         2514 45
         2520 <210> SEQ ID NO: 38
         2523 <211> LENGTH: 53
         2526 <212> TYPE: DNA
         2529 <213> ORGANISM: ARTIFICIAL SEQUENCE
         2535 <220> FEATURE:
         2538 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
         2541      OLIGONUCLEOTIDE
         2547 <400> SEQUENCE: 38
E--> 2550 ggccgcgtcg tcgtcgtcct tgtagtcggg gaccccgcag ccgaaggtgg    same
         2551 tac        53
         2629 <210> SEQ ID NO: 41
         2632 <211> LENGTH: 55
         2635 <212> TYPE: DNA
         2638 <213> ORGANISM: ARTIFICIAL SEQUENCE
         2644 <220> FEATURE:
         2647 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
         2650      OLIGONUCLEOTIDE
         2656 <400> SEQUENCE: 41
E--> 2659 ggccgctctt gctgcccct ttgatgatga tgacaagatc gttgggggct    same
         2660 atgct      55
         2666 <210> SEQ ID NO: 42
         2669 <211> LENGTH: 55
         2672 <212> TYPE: DNA
         2675 <213> ORGANISM: ARTIFICIAL SEQUENCE
         2681 <220> FEATURE:
         2684 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
         2687      OLIGONUCLEOTIDE
         2693 <400> SEQUENCE: 42
E--> 2696 ctagagcata gcccccaacg atcttgtcat catcatcaaa gggggcagca    same
         2697 agagc      55
         2703 <210> SEQ ID NO: 43
         2706 <211> LENGTH: 55
         2709 <212> TYPE: DNA
         2712 <213> ORGANISM: ARTIFICIAL SEQUENCE
         2718 <220> FEATURE:
         2721 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
         2724      OLIGONUCLEOTIDE
         2730 <400> SEQUENCE: 43
E--> 2733 ggccgctctt gctgcccct ttgatgatga tgacaagatc gttgggggct    same
         2734 attgt      55
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
     2740 <210> SEQ ID NO: 44
     2743 <211> LENGTH: 55
     2746 <212> TYPE: DNA
     2749 <213> ORGANISM: ARTIFICIAL SEQUENCE
     2755 <220> FEATURE:
     2758 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
     2761       OLIGONUCLEOTIDE
     2767 <400> SEQUENCE: 44
E--> 2770 ctagacaata gcccccaacg atcttgtcat catcatcaaa gggggcagca      same
     2771 agagc       55
     2777 <210> SEQ ID NO: 45
     2780 <211> LENGTH: 52
     2783 <212> TYPE: DNA
     2786 <213> ORGANISM: ARTIFICIAL SEQUENCE
     2792 <220> FEATURE:
     2795 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
     2798       OLIGONUCLEOTIDE
     2804 <400> SEQUENCE: 45                                          same
E--> 2807 ggccgctctt gctgccccct ttatcgaggg gcgcattgtg gagggctcgg
     2808 at          52
     2814 <210> SEQ ID NO: 46
     2817 <211> LENGTH: 52
     2820 <212> TYPE: DNA
     2823 <213> ORGANISM: ARTIFICIAL SEQUENCE
     2829 <220> FEATURE:
     2832 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
     2835       OLIGONUCLEOTIDE
     2841 <400> SEQUENCE: 46                                          same
E--> 2844 ctagatccga gccctccaca atgcgccect cgataaaggg ggcagcaaga
     2845 gc          52
     3280 <210> SEQ ID NO: 54
     3283 <211> LENGTH: 284
     3286 <212> TYPE: PRT
     3289 <213> ORGANISM: ARTIFICIAL SEQUENCE
     3295 <220> FEATURE:
     3298 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: HUMAN MH2
     3301       PROTEASE IN PFEK ZYMOGEN VECTOR
     3307 <400> SEQUENCE: 54
     3310 MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU
     3313   1                   5                  10                  15
     3319 VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS
     3322                  20                  25                  30
     3328 ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP
     3331           35                  40                  45
     3337 ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN
     3340       50                  55                  60
     3346 PRO TRP GLN ALA ALA LEU VAL MET GLU ASN GLU LEU PHE CYS SER GLY
     3349  65                  70                  75                  80
     3355 VAL LEU VAL HIS PRO GLN TRP VAL LEU SER ALA ALA HIS CYS PHE GLN
```

please
edit
amino acid
letters

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
3358                  85                  90                  95
3364 ASN SER TYR THR ILE GLY LEU GLY LEU HIS SER LEU GLU ALA ASP GLN
3367              100                 105                 110
3373 GLU PRO GLY SER GLN MET VAL GLU ALA SER LEU SER VAL ARG HIS PRO
3376          115                 120                 125
3382 GLU TYR ASN ARG PRO LEU LEU ALA ASN ASP LEU MET LEU ILE LYS LEU
3385      130                 135                 140
3391 ASP GLU SER VAL SER GLU SER ASP THR ILE ARG SER ILE SER ILE ALA
3394 145                 150                 155                 160
3400 SER GLN CYS PRO THR ALA GLY ASN SER CYS LEU VAL SER GLY TRP GLY
3403              165                 170                 175
3409 LEU LEU ALA ASN GLY ARG MET PRO THR VAL LEU GLN CYS VAL ASN
E--> 3410 VAL
E--> 3413              180                 185                 190
3419 SER VAL VAL SER GLU GLU VAL CYS SER LYS LEU TYR ASP PRO LEU TYR
E--> 3422          195                 200                 205
3428 HIS PRO SER MET PHE CYS ALA GLY GLY GLY HIS ASP GLN LYS ASP SER
E--> 3431      210                 215                 220
3437 CYS ASN GLY ASP SER GLY GLY PRO LEU ILE CYS ASN GLY TYR LEU GLN
E--> 3440 225                 230                 235                 240
3446 GLY LEU VAL SER PHE GLY LYS ALA PRO CYS GLY GLN VAL GLY VAL PRO
E--> 3449              245                 250                 255
3455 GLY VAL TYR THR ASN LEU CYS LYS PHE THR GLU TRP ILE GLU LYS THR
E--> 3458              260                 265                 270
3464 VAL GLN ALA SER SER ARG HIS HIS HIS HIS HIS HIS
E--> 3467          275                 280
3608 <210> SEQ ID NO: 59
3611 <211> LENGTH: 1103
3614 <212> TYPE: DNA
3617 <213> ORGANISM: ARTIFICIAL SEQUENCE
3623 <220> FEATURE:
3626 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID
3629      SEQUENCE OF HUMAN PROTEASE F IN CFEK2 ZYMOGEN
3632      VECTOR
3638 <400> SEQUENCE: 59
E--> 3641 gaattcacca ccatggcttt cctctggctc ctctcctgct gggccctcct
3642 gggtaccacc 60
E--> 3645 ttcggctgcg gggtccccga ctacaaggac gacgacgacg cggccgctct
3646 tgctgccccc 120
E--> 3649 tttgatgatg atgacaagat cgttgggggc tatgctctag aactcgggcg
3650 ttggccgtgg 180
E--> 3653 caggggagcc tgcgcctgtg ggattcccac gtatgcggag tgagcctgct
3654 cagccaccgc 240
E--> 3657 tgggcactca cggcggcgca ctgctttgaa acctatagtg accttagtga
3658 tccctccggg 300
E--> 3661 tggatggtcc agtttggcca gctgacttcc atgccatcct tctggagcct
3662 gcaggcctac 360
E--> 3665 tacaaccgtt acttcgtatc gaatatctat ctgagccctc gctacctggg
3666 gaattcaccc 420
```

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:56

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01032002\J015989.raw**

```
E--> 3669 tatgacattg ccttggtgaa gctgtctgca cctgtcacct acactaaaca
     3670 catccagccc 480
E--> 3673 atctgtctcc aggcctccac atttgagttt gagaaccgga cagactgctg
     3674 ggtgactggc 540
E--> 3677 tggggtaca tcaaagagga tgaggcactg ccatctcccc acaccctcca
     3678 ggaagttcag 600
E--> 3681 gtcgccatca taaacaactc tatgtgcaac cacctcttcc tcaagtacag
     3682 tttccgcaag 660
E--> 3685 gacatctttg gagacatggt ttgtgctggc aatgcccaag gcgggaagga
     3686 tgcctgcttc 720
E--> 3689 ggtgactcag gtggaccctt ggcctgtaac aagaatggac tgtggtatca
     3690 gattggagtc 780
E--> 3693 gtgagctggg gagtgggctg tggtcggccc aatcggcccg gtgtctacac
     3694 caatatcagc 840
E--> 3697 caccactttg agtggatcca gaagctgatg gcccagagtg gcatgtccca
     3698 gccagacccc 900
E--> 3701 tcctggtcta gacatcacca tcaccatcac tagcggccgc ttccctttag
     3702 tgagggttaa 960
E--> 3705 tgcttcgagc agacatgata agatacattg atgagtttgg acaaaccaca
     3706 actagaatgc 1020
E--> 3709 agtgaaaaaa atgctttatt tgtgaaattt gtgatgctat tgctttattt
     3710 gtaaccatta 1080
     3713 taagctgcaa taaacaagtt gac                          1103
```

Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:57

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01032002\J015989.raw**

```
L:31 M:270 C: Current Application Number differs, Replaced Application Number
L:34 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
L:82 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
M:254 Repeated in SeqNo=1
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:2
M:112 Repeated in SeqNo=2
M:254 Repeated in SeqNo=2
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
M:112 Repeated in SeqNo=3
M:254 Repeated in SeqNo=3
L:266 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
M:112 Repeated in SeqNo=4
M:254 Repeated in SeqNo=4
L:326 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
M:112 Repeated in SeqNo=5
M:254 Repeated in SeqNo=5
L:383 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:6
M:112 Repeated in SeqNo=6
M:254 Repeated in SeqNo=6
L:443 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:7
M:112 Repeated in SeqNo=7
M:254 Repeated in SeqNo=7
L:555 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:8
M:112 Repeated in SeqNo=8
M:254 Repeated in SeqNo=8
L:667 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:9
M:112 Repeated in SeqNo=9
M:254 Repeated in SeqNo=9
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:10
M:112 Repeated in SeqNo=10
M:254 Repeated in SeqNo=10
L:1242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:1719 M:112 C: (48) String data converted to lower case,
L:1755 M:112 C: (48) String data converted to lower case,
L:1791 M:112 C: (48) String data converted to lower case,
L:1827 M:112 C: (48) String data converted to lower case,
L:1863 M:112 C: (48) String data converted to lower case,
L:1899 M:112 C: (48) String data converted to lower case,
L:1935 M:112 C: (48) String data converted to lower case,
L:1971 M:112 C: (48) String data converted to lower case,
L:2007 M:112 C: (48) String data converted to lower case,
L:2043 M:112 C: (48) String data converted to lower case,
L:2079 M:112 C: (48) String data converted to lower case,
L:2115 M:112 C: (48) String data converted to lower case,
L:2151 M:112 C: (48) String data converted to lower case,
```

VERIFICATION SUMMARY   DATE: 01/03/2002
PATENT APPLICATION: US/10/015,989   TIME: 15:41:57

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

```
L:2187 M:112 C: (48) String data converted to lower case,
L:2223 M:112 C: (48) String data converted to lower case,
L:2259 M:112 C: (48) String data converted to lower case,
L:2295 M:112 C: (48) String data converted to lower case,
L:2331 M:112 C: (48) String data converted to lower case,
L:2367 M:112 C: (48) String data converted to lower case,
L:2403 M:112 C: (48) String data converted to lower case,
L:2439 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:35
M:112 Repeated in SeqNo=35
L:2476 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:36
M:112 Repeated in SeqNo=36
L:2513 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:37
M:112 Repeated in SeqNo=37
L:2550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:38
M:112 Repeated in SeqNo=38
L:2587 M:112 C: (48) String data converted to lower case,
L:2623 M:112 C: (48) String data converted to lower case,
L:2659 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:41
M:112 Repeated in SeqNo=41
L:2696 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:42
M:112 Repeated in SeqNo=42
L:2733 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:43
M:112 Repeated in SeqNo=43
L:2770 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:44
M:112 Repeated in SeqNo=44
L:2807 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:45
M:112 Repeated in SeqNo=45
L:2844 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:46
M:112 Repeated in SeqNo=46
L:2881 M:112 C: (48) String data converted to lower case,
L:2917 M:112 C: (48) String data converted to lower case,
L:2953 M:112 C: (48) String data converted to lower case,
L:2989 M:112 C: (48) String data converted to lower case,
L:3025 M:112 C: (48) String data converted to lower case,
L:3061 M:112 C: (48) String data converted to lower case,
L:3410 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54
M:332 Repeated in SeqNo=54
L:3503 M:112 C: (48) String data converted to lower case,
L:3641 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:59
M:254 Repeated in SeqNo=59
L:3752 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:60
M:254 Repeated in SeqNo=60
```